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235670.ST25 - US Sequence Listing
SEQUENCE LISTING

<110> KISHIMOTO, Takahide
SOGABE, Atsushi
OKA, Masanori

<120> MODIFIED SARCOSINE OXIDASE, PROCESS FOR PRODUCING THE SAME AND
REAGENT COMPOSITION USING THE SAME

<130> 235670

<150> PCT/JP2003/014423
<151> 2003-11-13

<150> JP2002-329427
<151> 2002-11-13

<150> JP2002-329428
<151> 2002-11-13

<150> JP2003-33641
<151> 2003-02-12

<160> 14

<170> PatentIn version 3.1

<210> 1
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<212> PRT
<213> Arthrobacter SP. TE1826

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Met Ser Ile Lys Lys Asp Tyr Asp Val Ile Val Val Gly Ala Gly Ser
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Met Gly Met Ala Ala Gly Tyr Tyr Leu Ser Lys Gln Gly Val Lys Thr
20 25 30

Leu Leu Val Asp Ser Phe His Pro Pro His Thr Asn Gly Ser His His
35 40 45

Gly Asp Thr Arg Ile Ile Arg His Ala Tyr Gly Glu Gly Arg Glu Tyr
50 55 60

Val Pro Phe Ala Leu Arg Ala Gln Glu Leu Trp Tyr Glu Leu Glu Lys
65 70 75 80

Glu Thr His His Lys Ile Phe Thr Lys Thr Gly Val Leu Val Phe Gly
85 90 95

Pro Lys Gly Glu Ala Pro Phe Val Ala Glu Thr Met Glu Ala Ala Lys
100 105 110

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Glu His Ser Leu Asp Val Asp Leu Leu Glu Gly Ser Glu Ile Asn Lys
115 120 125

Arg Trp Pro Gly Val Thr Val Pro Glu Asn Tyr Asn Ala Ile Phe Glu
130 135 140

Lys Asn Ser Gly Val Leu Phe Ser Glu Asn Cys Ile Arg Ala Tyr Arg
145 150 155 160

Glu Leu Ala Glu Ala Asn Gly Ala Lys Val Leu Thr Tyr Thr Pro Val
165 170 175

Glu Asp Phe Glu Ile Ala Glu Asp Phe Val Lys Ile Gln Thr Ala Tyr
180 185 190

Gly Ser Phe Thr Ala Ser Lys Leu Ile Val Ser Met Gly Ala Trp Asn
195 200 205

Ser Lys Leu Leu Ser Lys Leu Asn Ile Glu Ile Pro Leu Gln Pro Tyr
210 215 220

Arg Gln Val Val Gly Phe Phe Glu Cys Asp Glu Lys Lys Tyr Ser Asn
225 230 235 240

Thr His Gly Tyr Pro Ala Phe Met Val Glu Val Pro Thr Gly Ile Tyr
245 250 255

Tyr Gly Phe Pro Ser Phe Gly Gly Cys Gly Leu Lys Ile Gly Tyr His
260 265 270

Thr Tyr Gly Gln Lys Ile Asp Pro Asp Thr Ile Asn Arg Glu Phe Gly
275 280 285

Ile Tyr Pro Glu Asp Glu Gly Asn Ile Arg Lys Phe Leu Glu Thr Tyr
290 295 300

Met Pro Gly Ala Thr Gly Glu Leu Lys Ser Gly Ala Val Cys Met Tyr
305 310 315 320

Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe
325 330 335

Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe
340 345 350

Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys
355 360 365

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Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys
370 375 380

Gln Lys Glu Thr Ile
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atg gga atg gca gct ggg tac tat ctg tct aaa caa ggt gtt aaa aca 96
Met Gly Met Ala Ala Gly Tyr Tyr Leu Ser Lys Gln Gly Val Lys Thr
20 25 30
cta ttg gta gat tca ttt cat cct ccc cat aca aat ggc agc cat cat 144
Leu Leu Val Asp Ser Phe His Pro Pro His Thr Asn Gly Ser His His
35 40 45
ggc gat aca cgg atc att cgt cac gca tat ggc gaa gga aga gag tat 192
Gly Asp Thr Arg Ile Ile Arg His Ala Tyr Gly Glu Gly Arg Glu Tyr
50 55 60
gta ccg ttt gcc ttg aga gca caa gag tta tgg tat gaa tta gaa aag 240
Val Pro Phe Ala Leu Arg Ala Gln Glu Leu Trp Tyr Glu Leu Glu Lys
65 70 75 80
gag act cat cat aaa ata ttt aca aaa aca ggt gta ctc gtt ttt ggt 288
Glu Thr His His Lys Ile Phe Thr Lys Thr Gly Val Leu Val Phe Gly
85 90 95
cct aaa gga gaa gct cct ttc gtt gcc gaa aca atg gaa gcc gca aag 336
Pro Lys Gly Glu Ala Pro Phe Val Ala Glu Thr Met Glu Ala Ala Lys
100 105 110
gaa cat tca tta gat gtt gat tta cta gaa gga agt gaa ata aat aag 384
Glu His Ser Leu Asp Val Asp Leu Leu Glu Gly Ser Glu Ile Asn Lys
115 120 125
cgt tgg cca ggt gta acg gtt cct gag aat tat aat gct att ttt gaa 432
Arg Trp Pro Gly Val Thr Val Pro Glu Asn Tyr Asn Ala Ile Phe Glu
130 135 140
aaa aat tct ggt gtc tta ttt agt gaa aat tgt att cgc gct tac cgt 480
Lys Asn Ser Gly Val Leu Phe Ser Glu Asn Cys Ile Arg Ala Tyr Arg
145 150 155 160
gaa ttg gcg gaa gca aat ggt gcg aaa gtt cta acg tac aca ccc gtt 528
Glu Leu Ala Glu Ala Asn Gly Ala Lys Val Leu Thr Tyr Thr Pro Val
165 170 175

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gaa gat ttc gag att gcc gag gac ttc gtc aaa atc caa acc gcc tat Glu Asp Phe Glu Ile Ala Glu Asp Phe Val Lys Ile Gln Thr Ala Tyr 180 185 190	576
ggc tcc ttt aca gcc agt aaa tta att gtt agc atg ggc gct tgg aat Gly Ser Phe Thr Ala Ser Lys Leu Ile Val Ser Met Gly Ala Trp Asn 195 200 205	624
agc aaa ctg cta tca aaa tta aat att gaa atc cca ttg cag cca tac Ser Lys Leu Leu Ser Lys Leu Asn Ile Glu Ile Pro Leu Gln Pro Tyr 210 215 220	672
cgt caa gtt gtc gga ttc ttc gaa tgt gat gaa aaa aaa tat agc aat Arg Gln Val Val Gly Phe Phe Glu Cys Asp Glu Lys Lys Tyr Ser Asn 225 230 235 240	720
aca cat ggt tat ccg gcg ttc atg gtc gaa gtc cca act ggc atc tat Thr His Gly Tyr Pro Ala Phe Met Val Glu Val Pro Thr Gly Ile Tyr 245 250 255	768
tac gga ttt cca agc ttc ggc ggc tgc ggc ttg aaa ata ggc tat cat Tyr Gly Phe Pro Ser Phe Gly Gly Cys Gly Leu Lys Ile Gly Tyr His 260 265 270	816
acg tat ggt caa aaa atc gat cca gat acg att aat cgt gaa ttt ggt Thr Tyr Gly Gln Lys Ile Asp Pro Asp Thr Ile Asn Arg Glu Phe Gly 275 280 285	864
att tac ccg gag gat gaa ggc aat att cgc aaa ttc ctg gaa aca tat Ile Tyr Pro Glu Asp Glu Gly Asn Ile Arg Lys Phe Leu Glu Thr Tyr 290 295 300	912
atg ccg gga gca acc ggc gaa tta aaa agt ggc gca gtt tgc atg tac Met Pro Gly Ala Thr Gly Glu Leu Lys Ser Gly Ala Val Cys Met Tyr 305 310 315 320	960
aca aaa aca cct gat gag cat ttc gtg att gat tta cat cct caa ttc Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe 325 330 335	1008
tcg aat gtc gcg att gca gcc gga ttc tcc gga cat ggc ttt aaa ttc Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe 340 345 350	1056
tca agc gta gtt ggt gaa aca tta agt caa tta gct gta acc ggt aaa Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys 355 360 365	1104
aca gaa cac gat att tcc atc ttt tca atc aat cgc cct gct tta aaa Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys 370 375 380	1152
caa aaa gaa acg att Gln Lys Glu Thr Ile 385	1167

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<220>
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<210> 4
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235670.ST25 - US Sequence Listing

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